

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:52:13 ; Search time 301 Seconds  
(without alignments)  
8895.537 Million cell updates/sec

Title: US-10-643-829-1

Perfect score: 1431

Sequence: 1 ccgtccagacgtctcagcg.....ccggtacgcgacgtccttg 1431

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- Issued Patents\_NA:\*
- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*
  - 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*
  - 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*
  - 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*
  - 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*
  - 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*
  - 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*
  - 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*
  - 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*
  - 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	44378	3	US-09-949-016-12540 Sequence 12540, A
2	909.4	63.5	1237	3	US-09-007-678B-48 Sequence 48, Appl
3	703.6	49.2	84875	3	US-09-949-016-17334 Sequence 17334, A
4	703.6	49.2	84875	3	US-09-949-016-17335 Sequence 17335, A
5	703.6	49.2	84875	3	US-09-949-016-17336 Sequence 17336, A
6	703.6	49.2	84875	3	US-09-949-016-17337 Sequence 17337, A
7	703.6	49.2	85152	3	US-09-949-016-12665 Sequence 12665, A
8	703.6	49.2	85152	3	US-09-949-016-12666 Sequence 12666, A
9	703.6	49.2	85152	3	US-09-949-016-12667 Sequence 12667, A
10	703.6	49.2	85152	3	US-09-949-016-12668 Sequence 12668, A
11	701	49.0	3798	3	US-09-023-655-887 Sequence 887, Appl
12	281.2	19.7	512	3	US-09-949-016-4540 Sequence 4540, Ap
13	279.6	19.5	512	4	US-09-880-107-2282 Sequence 2282, Ap
14	279.4	19.5	9153	3	US-09-949-016-15183 Sequence 15183, A
15	249.2	17.4	187595	3	US-09-949-016-15546 Sequence 15546, A
16	247.8	17.3	422	3	US-09-397-787-186 Sequence 186, Appl
17	220.6	15.4	3227	3	US-09-976-594-775 Sequence 775, Appl
18	203.4	14.2	237	3	US-09-397-787-89 Sequence 89, Appl
19	189.4	13.2	211049	3	US-09-949-016-15770 Sequence 15770, A
20	180.6	12.6	309	3	US-09-313-294A-7018 Sequence 7018, Ap
21	177	12.4	6727	3	US-09-949-016-16282 Sequence 16282, A
22	163.4	11.4	464	3	US-09-774-528-63 Sequence 63, Appl
23	163.4	11.4	464	3	US-10-120-988-63 Sequence 63, Appl

C	24	146.4	10.2	2124	10	5428012-1	Parent No. 5428012
C	25	146.4	10.2	2124	10	5451506-1	Parent No. 5451506
C	26	143.6	10.0	103377	3	US-09-949-016-14089	Sequence 14089, A
	27	142.2	9.9	90541	3	US-09-759-359A-3	Sequence 3, Appl1
	28	142.2	9.9	90541	3	US-10-207-973-3	Sequence 3, Appl1
	29	142.2	9.9	90541	5	US-10-799-676-3	Sequence 3, Appl1
	30	142.2	9.9	156651	3	US-09-949-016-17349	Sequence 17349, A
	31	140.4	9.8	376	3	US-09-949-016-3441	Sequence 3441, Ap
C	32	114	8.0	1534	2	US-08-480-784-13	Sequence 13, Appl
C	33	114	8.0	1534	2	US-08-483-553-13	Sequence 13, Appl
C	34	114	8.0	1534	2	US-08-483-554B-13	Sequence 13, Appl
C	35	114	8.0	1534	2	US-08-483-554B-13	Sequence 13, Appl
C	36	114	8.0	1534	2	US-08-488-011B-13	Sequence 13, Appl
C	37	114	8.0	1534	3	US-08-850-727-13	Sequence 13, Appl
C	38	114	8.0	1534	7	PCT-US95-10202-13	Sequence 13, Appl
C	39	114	8.0	1534	7	PCT-US95-10203-13	Sequence 13, Appl
C	40	114	8.0	1534	7	PCT-US95-10220-13	Sequence 13, Appl
C	41	114	8.0	1924	2	US-08-480-784-14	Sequence 14, Appl
C	42	114	8.0	1924	2	US-08-483-553-14	Sequence 14, Appl
C	43	114	8.0	1924	2	US-08-487-002-14	Sequence 14, Appl
C	44	114	8.0	1924	2	US-08-483-554B-14	Sequence 14, Appl
C	45	114	8.0	1924	2	US-08-488-011B-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-12540  
Sequence 12540, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CI001307  
CURRENT APPLICATION NUMBER: US/09/949, 016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12540  
LENGTH: 44378  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(44378)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12540

Query Match 100.0%; Score 1431; DB 3; Length 44378;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CCGTCAGAACGCTCAGCAGCTCAGCAGCGCAGTTCAGCTTTTCCCTCTAC	60
DB	604	CCGTCAGAACGCTCAGCAGCTCAGCAGCGCAGTTCAGCTTTTCCCTCTAC	663
QY	61	ATTGACAGATGTGCTCCCATGTGACGTTGGCCAGACCTTGCACACAGCGCCA	120
DB	664	ATTGACAGATGTGCTCCCATGTGACGTTGGCCAGACCTTGCACACAGCGCCA	723
QY	121	AAAAGTTCAATTTTCACTGGCTGCTTTAATAAGGCATTGATCTTATCCCTGTA	180
DB	724	AAAAGTTCAATTTTCACTGGCTGCTTTAATAAGGCATTGATCTTATCCCTGTA	783
QY	181	GGTACCTCATAGTCTCTGCAAGATGAGGGCAGAGTATGATGCAAGGCAAGCTGGAGACGGA	240

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Db      784  GGTCACTCTAAGTCTCTGAGAAATGAGGCAAGTAGATGCAAGCAAGCTGGAGACGGA 843
Qy      241  GGCCATAGCCGGGGCGAGTGTGGGGCTGGGGCTCCGGACCGGGTCTACTCACCCGATG 300
Db      844  GGCCATAGCCGGGGCGAGTGTGGGGCTGGGGCTCCGGACCGGGTCTACTCACCCGATG 903
Qy      301  AAGTGAAGGTCTCACCCCAACGCGGCTTAGCTCTCTGGAAAGACCGAACACCTTGGCG 360
Db      904  AAGTGAAGGTCTCACCCCAACGCGGCTTAGCTCTCTGGAAAGACCGAACACCTTGGCG 963
Qy      361  GCAGCCGAGAAAGGGGTTCCACAGTTTAAATTATCTGTAATCCACGCTTACTGTT 420
Db      964  GCAGCCGAGAAAGGGGTTCCACAGTTTAAATTATCTGTAATCCACGCTTACTGTT 1023
Qy      421  GCCACGAAACCGCTGAGCAATAGCCTCTCAGAAATAGAAATCAAGACAGTCAGAGA 480
Db      1024  GCCACGAAACCGCTGAGCAATAGCCTCTCAGAAATAGAAATCAAGACAGTCAGAGA 1083
Qy      481  AGGCGCGGACAGAAAGAGCCTAGCATCTCTCGGGGCTCTGGGTTGGCCACCAGTCTCC 540
Db      1084  AGGCGCGGACAGAAAGAGCCTAGCATCTCTCGGGGCTCTGGGTTGGCCACCAGTCTCC 1143
Qy      541  CTTGGTGACATAAAAAGAAAGAGACGGAAGAAAGAAATTTACCTGAGTTCCGCCGTA 600
Db      1144  CTTGGTGACATAAAAAGAAAGAGACGGAAGAAAGAAATTTACCTGAGTTCCGCCGTA 1203
Qy      601  GCGCCCGCCCTCTCGCCTCTACGCTTCCAGTTGCGGCTTATTAAGTCAAGTAATGCTG 660
Db      1204  GCGCCCGCCCTCTCGCCTCTACGCTTCCAGTTGCGGCTTATTAAGTCAAGTAATGCTG 1263
Qy      661  TACCAAGGTCAGAATCGCCACCTGAGGCTGAATATCAGCGTAAGATAGTGTCCAAAGCA 720
Db      1264  TACCAAGGTCAGAATCGCCACCTGAGGCTGAATATCAGCGTAAGATAGTGTCCAAAGCA 1323
Qy      721  GTCTTAAGAAGAGTCCCATTAACCACTCTTCCGCCCTAATGAGGTCTCCAGTTAG 780
Db      1324  GTCTTAAGAAGAGTCCCATTAACCACTCTTCCGCCCTAATGAGGTCTCCAGTTAG 1383
Qy      781  GTAAATAAAAAGATGTGTGGAGGTGAGAGGAAAGAACTACTATTCCACATGCAATTGC 840
Db      1384  GTAAATAAAAAGATGTGTGGAGGTGAGAGGAAAGAACTACTATTCCACATGCAATTGC 1443
Qy      841  GGAACGAAAGGCTTGCGCCACACTGTCTTGAAACTGTAGTCTTATGAGAGGAACAT 900
Db      1444  GGAACGAAAGGCTTGCGCCACACTGTCTTGAAACTGTAGTCTTATGAGAGGAACAT 1503
Qy      901  CCAATACCAAAAGCGGCACAATTTCTACGGAATCCAGTGATAGATTGAGAGACCTCCG 960
Db      1504  CCAATACCAAAAGCGGCACAATTTCTACGGAATCCAGTGATAGATTGAGAGACCTCCG 1563
Qy      961  GGGCTTATACATGTCAACAGTAATGATTGAGTGTGTATGTTCTCTATCTTGAGAG 1020
Db      1564  GGGCTTATACATGTCAACAGTAATGATTGAGTGTGTATGTTCTCTATCTTGAGAG 1623
Qy      1021  CAGAGACTAGGCCAAAAAAGATACTCACTCCTAGAGAGACTAGATTCCCATCCAG 1080
Db      1624  CAGAGACTAGGCCAAAAAAGATACTCACTCCTAGAGAGACTAGATTCCCATCCAG 1683
Qy      1081  CCCCACGAGTCTCGGGCAAGTACTCTTAAGGTCAAGTGGCTGCGGGACGCAAGTGGGC 1140
Db      1684  CCCCACGAGTCTCGGGCAAGTACTCTTAAGGTCAAGTGGCTGCGGGACGCAAGTGGGC 1743
Qy      1141  GCCGAATTTGCTGGGGAAGGGAATCCGCTCTGGCCCATCTGCGCACTCTAGTTT 1200
Db      1744  GCCGAATTTGCTGGGGAAGGGAATCCGCTCTGGCCCATCTGCGCACTCTAGTTT 1803
Qy      1201  CGCCCTCAGCCTCAATGTTTGTATTTGTGTTGCGGTTCAGGTGCTTCTGCCGCC 1260
Db      1804  CGCCCTCAGCCTCAATGTTTGTATTTGTGTTGCGGTTCAGGTGCTTCTGCCGCC 1863
Qy      1261  CATGACGCAATCTCAACCAATCAATGCGTGTGTTTGAAGGACAAGTGTGAGAGC 1320
Db      1320  CATGACGCAATCTCAACCAATCAATGCGTGTGTTTGAAGGACAAGTGTGAGAGC 1320
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Db      1864  CATGACGCAATCTCAACCAATCAATGCGTGTGTTTGAAGGACAAGTGTGAGAGC 1923
Qy      1321  CAATCATCTTGCGGAACACTCGGAGAAACAGGGGACTAGTACTGTCTTATCCGCATG 1380
Db      1924  CAATCATCTTGCGGAACACTCGGAGAAACAGGGGACTAGTACTGTCTTATCCGCATG 1983
Qy      1381  TTAGATTACCCCAAGGATAGCGGACAGACCGGTAGCGGACGGTCTTG 1431
Db      1984  TTAGATTACCCCAAGGATAGCGGACAGACCGGTAGCGGACGGTCTTG 2034

RESULT 2
US-09-007-678B-48
; Sequence 48, Application US/09007678B
; Patent No. 6342483
; GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: PAGE, DAVID L.
; APPLICANT: OBERMILLER, PATRICE S.
; APPLICANT: ROBINSON-BENION, CHERYL L.
; APPLICANT: THOMPSON, MARLYN E.
; TITLE OF INVENTION: METHOD FOR DETECTION AND TREATMENT OF BREAST CANCER
; FILE REFERENCE: Attorney Docket No. 6342483 1242-1-2-2
; CURRENT APPLICATION NUMBER: US/09/007, 678B
; CURRENT FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: 08/373, 799
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: 08/182, 961
; PRIOR FILING DATE: 1994-01-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Microsoft WordPad
; SEQ ID NO 48
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-007-678B-48

Query Match      63.5%; Score 909.4; DB 3; Length 1237;
Best Local Similarity 94.0%; Pred. No. 6.6e-277;
Matches 999; Conservative 0; Mismatches 36; Indels 28; Gaps 4;

Qy      381  CACAGTTTAAATTATCTGTAATTCACGCTTACTGTGCAAGAA----- 429
Db      131  CGCAGTTTAAATTATCTGTAATTCACGCTTACTGTGCAAGAAAGGGCT 190
Qy      430  ACCGTGAGCAATAGCCTCTCAGAAATAGAAATCAAGACAGTCAGAGAAAGGGCGGA 489
Db      191  ACCGTAGAGCAGCAGCCTCTCAGAAATAGAAATCAAGTACATCAGAGAAAGGAGGA 250
Qy      490  CAGAAAGAGCCTAGCATCTCTGGGGCTTGGGTTGGCCACCAGTCTCCCTGG-TGA 548
Db      251  CAGAAAGAGCAGCGCTCTCTGGGGCTTGGGTTGGCCACCAGTCTCCCTGGATGA 310
Qy      549  CATAAAAAGAAAGAGACGGAAGAAAGAAATTTACTAGTTCGCCGTAAGCGCCCGC 608
Db      311  CGTAAAGAAAGAGACGGAAGAAAGAAATTTACTAGTTCGCCGTAAGCGCCCGC 370
Qy      609  CCTCTCGCCTTACGCTTCCAGTTGCGGCTTATTAAGTCAAGTAATGCTGTACCAAGG 668
Db      371  CCTCTCGCCTTACGCTTCCAGTTGCGGCTTATTAAGTCAAGTAATGCTGTACCAAGG 430
Qy      669  TCAGATCGCACTGAGGCTGAATATACGCGTAAGTAGTGTCCAAGCAGTCTTAAG 728
Db      431  TCAGATCGCACTGAGGCTGAATATACGCGTAAGTAGTGTCCAAGCAGTCTTAAG 490
Qy      729  AAGAGTCCCATTAACCCCACTCTTCCGCCCTAATGAGAGTCTCAGTTAAGTAAATA 788
Db      491  AAGAGTCCCATTAACCCCACTCTTCCGCCCTAATGAGAGTCTCAGTTAAGTAAATA 550
Qy      789  AAGATGTGTGGAGGTGAGGGAAGAACTAATTTCCACATGCAATTCGGAACGA 848
Db      551  AAGATGTGTGGAGGTGAGGGAAGAACTAATTTCCACATGCAATTCGGAACGA 610
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QY	849	AGGCTTGGCCACACACTGTTCTCCCTTGGAACCTGTAGTCTTATGAGAGGAACATCCAAATACC	908
Db	611	AGGCTTGGCCACACACTGTTCTCCCTTGGAACCTGTAGTCTTATGAGAGGAACATCCAAATACC	670
QY	909	AAAGCGGGCACAATTCTCACGGAAATCCAGTGATAGATTGGAACCTCCGGGCTTAT	968
Db	671	AAAGCGGGCACAATTCTCACGGAAATCCAGTGATAGATTGGAACCTCCGGGCTTAT	730
QY	969	ACATGTCAACAGTAATGATGAGTGTGTATGTTCTCCTATCTTGAGAGCAGACT	1028
Db	731	ACATGTCAACAGTAA-----TATGGGTTGTATGTCTCCTATCTTGAGAGCAGACT	785
QY	1029	AGGCCAAAAAAGATACCTTACAACCTCTAGGAAGACTACGATTCCTATCCAGCCCCACGA	1088
Db	786	AGGCCAAAAAAGATA-----TAGGAAGACTACGATTCCTATCCAGCCCCACGA	834
QY	1089	GTCCTGGGCAAGTAGTCTCTTAAGTCAAGTGGCCCTGCGGGACGACAGTGGCGCCGAATT	1148
Db	835	GTCCTGGGCAAGTAGTCTCTTAAGTCAAGTGGCCCTGCGGGACGACAGTGGCGCCGAATT	894
QY	1149	TGCCTGGGGAAGGGGAATCCGCTCTGGCCACACATCTGCCACTCCTAGTTCGCCCTC	1208
Db	895	TGCCTGGGGAAGGGGAATCCCTCTCTGGTCACATCTGCCACTCCTAGTTCGCCCTC	954
QY	1209	AGCCTCAATGTTGTTATTTGTTGTTCTGGGTTCAAGTTGCTTCTGCCCCCCTCATCAG	1268
Db	955	AGCATCAATGTTGTTATTTGTTGTTCTGGGTTCAAGTTGCTTCTGCCCCCCTCATCAG	1014
QY	1269	CAATCTCCACCAATCAATGCGGTGTCGTTTGAAGGACAAGTGAGAGCCAAATCATC	1328
Db	1015	CAATCTCCACCAATCAATGCGGTGTCGTTTGAAGGACAAGTGAGAGCCAAATCATC	1074
QY	1329	TTGGCGAACACTCGAGAAACAGGGGACTAGTTACTGTCTTTATCCGCCATGTTAGATTC	1388
Db	1075	TTGGCGAACACTCGAGAAACAGGGGACTAGTTACTGTCTTTATCCGCCATGTTAGATTC	1134
QY	1389	ACCCCAACAGGATAGCGGCAAGCCGTTAGCGGACGGTCTTG 1431	
Db	1135	ACCCCAACAGGATAGCGGCAAGCCGTTAGCGGACGGTCTTG 1177	

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RESULT 3
US-09-949-016-17334/C
; Sequence 17334, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17334
; LENGTH: 84875
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17334

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Query Match	49.2%	Score 703.6;	DB 3;	Length 84875;
Best Local Similarity	85.0%	Pred. No. 1e-210;		
Matches 910;	Conservative	0;	Mismatches 109;	Indels 51;
				Gaps 9;

QY 381 CACAGTTTAAATTATCTGTAATCCACGCTTTACTGTGTCACGGAA----- 429

Db	1732	CGCAGTTTAAATTTA	1CTGTAATTCCCGCGCTTTTCCGTTGCCACGGAAACCAAGGGGCT	1673
QY	430	ACCGCTGAGCAATAGCCTCTCAGAA	TAGAAAATCAAGACACAGTCAAGAGGCGGGGA	489
Db	1672	ACCGCTAAGCAGACGCTCTCAGAA	TACGAAATCAAGGTACAAATCAGAGATGGAGGGA	1613
QY	490	CAGAAAGAGCCTAGCATCTCTCGGG	CTTGGGTTGGCCACCAGTCTCCCTGG-TGA	548
Db	1612	CAGAAAGAGCCAGCGTCTCTCGGG	CTGTGGATTTGGCCACCAGTCTGCCCCGGATGA	1553
QY	549	CATAAAAAGAAAGAGACGGAAAG	AGAAATTTCTACCTGAGTTCCGCGTAAAGCGCCCGC	608
Db	1552	CGTAAAGAGAAAGAGACGGAAAG	AGAAATTTCTACCTGAGTTTGCCTAAAGTGCTGC	1493
QY	609	CCTCTCGCCTTACGCTTCCAGTTG	CGGCTTATTAAGTCACAGTAATTTGCTGTACCAAG	668
Db	1492	CCTTAGCCCTTACTCTTCCAGTTG	CGGCTTATTTGCATCACAGTAATTTGCTGTACGAAG	1433
QY	669	TCGAATCGCCACCTGAGGCTGAA	TATACCGTAAAGTAGTGTCCAAAGCAGTCTTAAG	728
Db	1432	TCGAATCGCTAAC-----	-----TATTGTCCAAAGCAGTCTTAAG	1397
QY	729	AAGAGTCCCATTAACCCCACTCTT	CCGCCCTAATGAGAGTCTCCAGTTAAGTAAATAA	788
Db	1396	AAGAGTCCCAATCCCCCACTCTT	CCGCCCTAATGAGAGTCTCCAGTTCCGTAATAAT	1337
QY	789	AAGATTTGTTGGAGGTGAGGGAAG	-----AACTACTATTTCCAACATGCATTGGCGA	843
Db	1336	AAGTAATAAGATTTGTTGGGGGG	GTGAGGGAATAATATTTCCAGCATGCGTTGGCGA	1277
QY	844	ACGAAAGGCTTTGGCCACACACTG	TTCCCTTGGAAACTGTAGTCTTATGAGAGGAACATCCA	903
Db	1276	ATGAAGGTTTCGCCACAGTGTCTT	AGAAACTGTAGTCTTATGAGAGGAACATCCA	1217
QY	904	ATACCAAAAGGGGSCACAATTCT	CACGGAAATCCAGTGATAGATTGGAGACTTCCGCGGG	963
Db	1216	ATACCAAGGCGGSCACAATTCTC	ACGGAAATCCAGTGATAGATTGGAGACTTGTGCGCG	1157
QY	964	CTTATACATGTCAACAGTAATGA	ATTGGAAGTGTGTTATGTTCTCTATCTTGAGAGCAG	1023
Db	1156	CTTGTACTTGTCAACAGTTATGA	CTGAG-----TGTATGTTTTCGTATTTTGAAAGCAG	1100
QY	1024	AGACTAGGCCAAAAAAGATACCT	CAACTC-CTAGGAAGCTACGATTTCCCATCCAGCC	1082
Db	1099	AAACTAGGCTTAAAAAGATACCT	CAACTCTTTAGGAGACTACATTTCCCATCCAGCC	1040
QY	1083	CCACAGTCTCGGGCAAGTAGTCT	CTTAAGGTCAGTGGCCTCGCGGAGCCGACAGTGGGCGC	1142
Db	1039	CCAGAGTCTGGGGCAAGTAGTCT	GTAAAGTCAGTGGCCTCGCGGAGCCGACAGTGAAGCGC	980
QY	1143	CGAATTTGCTGGGGAAAGGGGAAA	TCCGCTCTGGCCACATCTGCGCACTCCTAGTTCGG	1202
Db	979	CGAATTTGCTGGGGCAAGGAAATG	CGCTCTGCCCCCATGTCTGCGCACTCGTAGTTCCA	920
QY	1203	CCCCCAGCCTCAATGTTTGTTAT	GTGTTGTTGCGGTTCAAGTTGCTTCTGCCCCG-CCCC	1261
Db	919	CCCCCAGCCCCCAGTGTGTTGTTA	---TTTTTCGGGTTCAAGCTTGTGTTGCCCCGCTCTCC	863
QY	1262	ATGAGCGCAATCTCCACCAATCA	ATGGCGTGTGCTTTTGAAGGACAAGTGTGAGAGCC	1321
Db	862	GTGAGCGCAATCGCCACCACTCA	ATGGGGTGTGCTTTTGAAGGACAAGTGTGAAGAGCC	803
QY	1322	AATCATCTTGGCGAACACTCGAG	AAACAGGGGACTAGTTACTGCTTTATCCGCCATGT	1381
Db	802	AATCTTCTTGGCGAAAACCGCGA	GAAC--GGGACTAGTTACTGCTTTGTCCGCCATGT	745
QY	1382	TAGATTCACCCCACAGGGATAG	CGGCGCAGAGCCGGTAGCCGACGGTCTTG	1431
Db	744	TAGATTCACCCCACAGAGATAG	CGGCGCAGAGCTGGCAGCGGACGGTCTTTG	695

RESULT 4  
US-09-949-016-17335/c



```

; Sequence 17335, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17335
; LENGTH: 84875
; TYPE: DNA
; ORGANISM: Human
US-09-016-17335

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Query Match	49.2%;	Score 703.6;	DB 3;	Length 84875;
Best Local Similarity	85.0%;	Pred. No. 1e-210;		
Matches 910;	Conservative 0;	Mismatches 109;	Indels 51;	Gaps 9;

Oy	381 CACAGTTTAAATTATCTGTAATTCCCA CGCCTTACTGTGGCCA GGA----- 429
Db	1732 CGCAGTTTTAATTATCTGTAATTCGCCGCCTTTCCGTTGCCA CGGAACCAGA GGCT 1673

Qy 430 ACCGCTGAGCAATAGCCTCTCAGAATAGGAAATCAAGACACAGTCAGAGGAAGGCCGGA 489

Db 1672 ACCGCTAAGCAGCAGCCTCTCAGAATACGAATCAAGGTACATCAGAGGATGGGAGGGA 1613

DY 490 CAGAAAGACCTAGCATCTCTCGGGGCTCTGGGTGGCCACCAGTCTCCTGG-TGA 548

Dδ 1612 CAGAAAGACCAAGCTCTCTCGGGGCTCTGATTGGCCACCAGTCTGCCCGCATGA 1553

Dy 549 CATAAAAGAAAGACGGAALAGAAGATTCTACTGACTTCGCCGTAAAGCGCCGC 608

Db 1552 CGTAAAGGAAAGACGGAAGAGAATTTCTACCAGTTTGCCATAAAGTGCCTC 1493

Dy		609 CCTCTGCCCTACGCTCCAGTTCGGCTATTACGCACAGATAATGCTGTACAAGG	668
Dδ	1492 CCTTAGCCTTA	CTTCCAAGTGCGGCTATTGCATCACAGTAATGCTGTACGAAGG	1433

QY 669 TCAGATCGGCACCTGAGGCTGAAATATCAGCGTAAGTAAGTGTCCAAAGCAGTCTTAAG 728  
 |||||  
 DB 1432 TCAGATCGCTACC-----TATTGTCCAAAGCAGTCTTAAG 1397  
 |||||

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QY      729 AAGAGGTCCCATTACCCCACTTTCCGCCCTAATGAGGTCTCCAGTTTAGGTAATAA 788
      |||
Db      1396 AAGAGGTCCCAATCCCACTCTTCCGCCCTAATGAGGTCTCCAGTTTCGGTAATAT 1337

```

QY 789 AAGGATTGTGGAGCGTGGAGGGAAG-----AACTACTATTTCCACATGCATTGCCGA 843  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1336 AAGTAATAAGATTGTGGGGGGGTGGAGGGAATAATTATTCACGATGCGTTGCCGA 1277

Oy 844 ACGAAGGCGCTGGCCACACTGTTCTTGGAAACTGTAGCTTTATGAGAGGAACATCCA 903  
 Db 1276 ATGAAGGCTTCGCCACAGTGTCTTAGAAACTGTAGTCTTATGAGAGGAACATCCA 1217

Dy 904 ATACCAAGCGGCACAATTCTACGGAATCCAGTGCATAGATTGGAGACCTCCGGG 963

Dd 1216 ATACCAGAGCGGCACAATTCTACGGAATCCAGTGCATAGATTGGAGACCTGTGCGG 1157

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Qy      964 CTATACATGTCAACAGTAATGGATTGAGTGTGTTATGTTCTCCATCTTGAGACAG 1023
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     1156 CTGTACTTGTCAACAGTTATGCGACTGCAG--TGTTATGTTTCGTATTGGAACGAG 1100
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1024 AGACTAGGCCAAAAAGATACCTACACTC-CTAGSAGACTAGATCCCATCCAGCC 1082

Db 1099 AAAC TAGGCCTTAAAAAGATACGTACAACCTCTTTAGGGAGACTACAAATTC CATCCAGCC 1040

Qy 1083 CCACGAGTCTCGGGCAAGTAGTCTCTAAGGTCAGTGGCC TCGGGGACGCA GTGGCGC 1142

Db 1039 CCAGAGTCTGGGGCAAGTAGTCTGTAAAGTCA GTGGCC TCGGGGACGCA GTAGCGC 980

Qy 1143 CGAATTTGCTGGGGAGGGAAATCCGCTCTGGCCCA CATCTGCGCACTCCTAGTCCG 1202

Db 979 CGAATTTGCTGGGGCAGGGGAAATCGGCTCTGGCCCATGTCTGCGCACTCGTAGTTCCA 920

Qy 1203 CCCCTCAGCCTCAATGTTTGTATTGTTGTTCCGGGTT CAGGTTGCTTCTGCCCG -CCCC 1261

Db 919 CCCCTCAGCCCCCAGTGTGTTA--TTT TTTCCGGGTT CAGGCTTGTCTTTTGCCCCGTC TC 863

Qy 1262 ATCGACGCAATCTCCACCAATCAATGCGGTGTCGTTT TGAGGGACAAGTGTGAGAGCC 1321

Db 862 GTCGACGCAATCGCCACCAAGTCAATGGGGTGTGCTTTTGAGGGACAAGTGTAAGAGCC 803

Qy 1322 AATCATCTTGGCGAACACTCGAGAGAAACAGGGGACTAGTACTGCTTTATCCGCCATGT 1381

Db 802 AATCTTCTTGGCGAAAAACGCGAGAAAC--GGGACTAGTACTGCTTTGTCCGCCATGT 745

Qy 1382 TAGATTCACCCCACAGGAGTAGCGGCAGAGCCGGTAGCGGACGGTCTTG 1431

Db 744 TAGATTCACCCCACAGAGATAGCGGCAGAGCTGGCAAGCGGACGGTCTT TG 695

RESULT 5  
US-09-949-016-17336/c  
; Sequence 17336, Application US/09949016

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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

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; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14
```

;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIORITY CLAIM: YES

```

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1234

```

```

; LENGTH: 84875
;
; TYPE: DNA
; ORGANISM: Human
;

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Query Match	49.2%;	Score 703.6;	DB 3;	Length 84875;
Best Local Similarity	85.0%;	Pred. No. 1e-210;		

381 CACAGTTTAAATTATCTGTAATCCACGCTTACTGTGCACGAA----- 429

430 ACCGCTGACCAATAGCCTCTCAGAAATGGAATCAAGACACAGTCAGAGGAAGGCGGGA 489

[illegible]

Qy 549 CATAAAGAAGACGGAAGAATTCTACTGATTCGCCGTAAAGCGCCGC 608  
| | | | | | | | | | | | | | | | | | | | |  
Ob 1EE2 CCTTATTTCTCATCAGCGGATCAAGGATATTTCTTACCTGAGCTTGCCATTAAGGTCCTGGC 1493

609 CCTTCGGCTCTACGCTTCAGTTGGGCTATTACGTCAAGTAATTGCTGTACCAAG 668



DB 862 GTGACGCAATCGCCACACTCAATGGGTGTCGTTTGAGGGACAAAGTGTAGAGCC 803  
QY 1322 AATCATCTTGGCGAACACTCGGAGAAAAGGGGACTAGTACTGCTTTATCCGCATGT 1381  
DB 802 AATCTTCTTGGCGAAAAGCGGAGAAAC--GGGACTAGTACTGCTTTGTCGCCCATGT 745  
QY 1382 TAGATTCAACCCACAGGATAGCGGACAGACCGGTAGCGGACGGTCTTG 1431  
DB 744 TAGATTCAACCCACAGAGATAGCGGACAGACGTGCGACGCGACGCTTTG 695

## RESULT 7

US-09-949-016-12665/c  
; Sequence 12665, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12665  
; LENGTH: 85152  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12665

Query Match 49.2%; Score 703.6; DB 3; Length 85152;  
Best Local Similarity 85.0%; Pred. No. 1e-210;  
Matches 910; Conservative 0; Mismatches 109; Indels 51; Gaps 9;

QY 381 CACAGTTTAAATTTATCTGTAAATCCACGCTTACTGTGCGACGAA----- 429  
DB 2009 CGCAGTTTAAATTTATCTGTAAATCCCGGCTTTCCGTTGCCACGAAACCAAGGGCT 1950  
QY 430 ACCGCTGACCAATAGCCTCTCAGAAATAGAAATCAAGACACAGTCAGAGGAGCGGA 489  
DB 1949 ACCGCTAAGCAGCAGCCTCTCAGAAATAGAAATCAAGTACATCAGAGATGGAGGGA 1890  
QY 490 CAGAAAGAGCCTAGCATCTCTCGGGCTCTGGGTGGCCACCCAGTCTCCCTGG-TGA 548  
DB 1889 CAGAAAGAGCCCAAGCGTCTCTCGGGCTCTGATTGGCCACCCAGTCTCCCGGATGA 1830  
QY 549 CATAAAAAGAAAGAGACGGAAGAAAGAAATTTACTGAGTTGCGCGTAAAGCGCCGC 608  
DB 1829 CGTAAAAAGAAAGAGACGGAAGAAAGAAATTTACTGAGTTGCGCATAAAGTGCCTGC 1770  
QY 609 CCTCTGCGCTCTAGCCTTCCAGTTGCGGCTTATTACGTCAGATAATTGCTGTACCAAG 668  
DB 1769 CCTCTAGCCTCTACTCTTCCAGTTGCGGCTTATTGATCAGTAATTGCTGTACCAAG 1710  
QY 669 TCAGAAATCGCCACCTGAGGCTGAATATCAGCGTAAGATGTCCAAAGCAGTCTTAAG 728  
DB 1709 TCAGAAATCGCTACC-----TATTGTCCAAAGCAGTCTTAAG 1674  
QY 729 AAGAGTCCCATTTACCCCACTTTTCCGCCCTAATGAGGTCTCCAGTTAGTAATAA 788  
DB 1673 AAGAGTCCCAATCCCCCACTTTTCCGCCCTAATGAGGTCTCCAGTTCCGTAATAAT 1614  
QY 789 AAGATTGTTGGAGGTGAGGAAAG-----AACTACTATTTCCAAATGATGATGGCGA 843  
DB 1613 AAGTATAAGATTGTTGGGGGGTGGAGGAAATATATTTTCCAGCATGCGTTGGCGGA 1554

QY 844 ACGAAGGCTTGGCCACACTGTTCTTGGAACCTGTAGTCTTATGAGAGAAACATCCA 903  
DB 1553 ATGAAGGTCTTCCGCCACAGTGTCTTGAACCTGTAGTCTTATGAGAGAAACATCCA 1494  
QY 904 ATACCAAGGGGCACAATTTCTACGGAATCCAGTGTAGATGAGAGACTCCGGGG 963  
DB 1493 ATACCAAGGGGCACAATTTCTACGGAATCCAGTGTAGATGAGAGACTCCGGGG 1434  
QY 964 CTTATACATGTCAACAGTAATGATGAGTGTGTTATGTTCTCTACTTGAAGACAG 1023  
DB 1433 CTGTACTGTCAACAGTATGAGTGTGAG--TGTATGTTTCTGTAATTTGAAGACAG 1377  
QY 1024 AGACTAGGCCAAAAAGATACCTACATC-CTAGGAAGACTACGATTCACAGCC 1082  
DB 1376 AAACCTAGGCTTAAAAAGATACGTACACTCTTATGAGAGACTACATTCACAGCC 1317  
QY 1083 CCACGAGTCTCGGGCAAGTAGTCTCTTAAGTCAAGTGGCTCGGGGACGCAAGTGGCGC 1142  
DB 1316 CCAGAGTCTGGGGCAAGTAGTCTCTTAAGTCAAGTGGCTCGGGGACGCAAGTGGCGC 1257  
QY 1143 CGAATTTGCTGGGGAGGGAATCCGCTCGGCCACATCTGCGCACTCTAGTTCCG 1202  
DB 1256 CGAATTTGCTGGGGAGGGAATCCGCTCGGCCACATCTGCGCACTCTAGTTCCA 1197  
QY 1203 CCCCTCAGCCTCAATGTTGTTATGTTGTTGCGGTTCAAGTGTCTTGCCTCCG-CCCC 1261  
DB 1196 CCCCTCAGCCTCAGTGTGTTA---TTTTCGGGTTCAAGTGTCTTGCCTCCGCTCC 1140  
QY 1262 ATCGACCAATCTCCACCAATCAATGCGGTGCTGTTTGAAGGACAAGTGTGAGAGCC 1321  
DB 1139 GTCGACGCAATCGCCACCAATGAGGTGCTGTTTGAAGGACAAGTGTGAGAGCC 1080  
QY 1322 AATCATCTTGGCGAACAACCTCGGAGAAACAGGGGACTAGTACTGTTATCCGCATGT 1381  
DB 1079 AATCTTCTTGGCGAAAAGCGGAGAAAC--GGGACTAGTACTGTTTGTCCGCATGT 1022  
QY 1382 TAGATTCAACCCACAGGATAGCGGACAGACCGGTAGCGGACGGTCTTG 1431  
DB 1021 TAGATTCAACCCACAGAGATAGCGGACAGAGCTGGCAGCGGACGGTCTTG 972

## RESULT 8

US-09-949-016-12666/c  
; Sequence 12666, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12666  
; LENGTH: 85152  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12666

Query Match 49.2%; Score 703.6; DB 3; Length 85152;  
Best Local Similarity 85.0%; Pred. No. 1e-210;  
Matches 910; Conservative 0; Mismatches 109; Indels 51; Gaps 9;

QY 381 CACAGTTTAAATTTATCTGTAAATCCACGCTTACTGTGCGACGAA----- 429  
DB 2009 CGCAGTTTAAATTTATCTGTAAATCCCGGCTTTCCGTTGCCACGAAACCAAGGGCT 1950



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QY 430 ACCGCTGACATAGCCTCTCAGATAGGAATCAAGACAGTCAAGAGAGGCGGGA 489
DB 1949 ACCGCTAAGCAGCAGCCTCTCAGAAATCAAGATCAAGTCAATCAGAGATGGAGGGA 1890
QY 490 CAGAAAGAGCCTAGCATCTCTCGGGGCTCTGGGTTGGCCACCAGTCTCCCTGG-TGA 548
DB 1889 CAGAAAGAGCAGCCTCTCTCGGGGCTCTGATGGCCACCAGTCTGCCCGGAGTA 1830
QY 549 CATAAAAAGAAAGAGAGGAAAGAAAGATTTCTACTGAGTTGCCGTAAGCCCGCC 608
DB 1829 CGTAAAGAGAAAGAGAGAGAGAAATTTCTACTGAGTTGCCATAAAGTGCCTGC 1770
QY 609 CCTCTGCGCTTACGCTTCCAAGTTGGGCTTATACGTACAGTAATGCTGTACCAAG 668
DB 1769 CCTCTAGCCTTACTCTTCCAGTTGCGGCTTATGATCAAGTAATGCTGTACGAAG 1710
QY 669 TCAGAAATCGCCACCTGAGGCGCTGAATATCAGCGTAAGATGTCCTCAAGCAGTCTTAAG 728
DB 1709 TCAGAAATCGCTACC-----TATTGTCCAAAGCAGTCTTAAG 1674
QY 729 AAGAGTCCCATTAACCCCACTCTTCCGCCCTTAATGAGGTCTCCAGTTAGTAAATAA 788
DB 1673 AAGAGTCCCAATCCCCCACTCTTCCGCCCTTAATGAGGTCTCCAGTTAGTAAATAA 1614
QY 789 AAGATGTGTGGAGGTGAGGGAAG-----AACTACTATTCCCAACATGATGCGGA 843
DB 1613 AAGTAATAGATTTGTTGGGGGGGTGAGGGAATTAATTTTCCAGCATGCGTTGCGGA 1554
QY 844 ACGAAAGCGCTTGGCCCACTGTTCTTGGAAACTGTAAGTTATGAGAGGAACATCCA 903
DB 1553 ATGAAAGGTCTTCCGCCACAGTGTCTTGAATACTGTAAGTTATGAGAGGAACATCCA 1494
QY 904 ATACCAAGCGGCGCACAATTTCTACGGAATTCAGTGATAGATGAGACCTCGCGGG 963
DB 1493 ATACCAAGCGGCGCACAATTTCTACGGAATTCAGTGATAGATGAGACCTCGCGGG 1434
QY 964 CTATATCATGTCAACAGTAATGATGATGTTGTTATGTTCTCTTAATTTGAGAGCAG 1023
DB 1433 CTGTATCTGTCAACAGTATGACTGGAG---TGTATGTTTCCATTTTGAAAGCAG 1377
QY 1024 AAGACTAGGCCAAAAAGATACCTACAATC-CTAGGAGACTACATTCCTCCATCCAGCC 1082
DB 1376 AACTAGGCTTAAAAAGATACCTACAATCCTTTAGGAGACTACATTCCTCCATCCAGCC 1317
QY 1083 CCAAGAGTCTCGGCGCAAGTAGTCTCTAAGGTCAAGTGGCTCGGCGGAGCGAGTGGCGG 1142
DB 1316 CCAAGAGTCTCGGCGCAAGTAGTCTCTAAGGTCAAGTGGCTCGGCGGAGCGAGTGGCGG 1257
QY 1143 CGAATTTGCTGGGGAAGGGAATCCGCTCTGGCCCAATCTGGCACTCCTAGTTCGG 1202
DB 1256 CGAATTTGCTGGGCGAGGGAATCCGCTCTGGCCCAATCTGGCACTCCTAGTTCGA 1197
QY 1203 CCCCTCAGCCTCAATGTTGTTATGTTGTTGCGGTTCAAGTTGCTTCTGCCCG-CCCC 1261
DB 1196 CCCCTCAGCCTCAAGTGTGTTA---TTTTTGGGTTCAAGTTGCTTCTGCCCGTCTCC 1140
QY 1262 ATGAGCGCAATCTCCACCAATCAATGCGGTGTCGTTTGAAGGACAAGTGTGAGAGCC 1321
DB 1139 GTGAGCGCAATCGCCACCAATCAATGCGGTGTCGTTTGAAGGACAAGTGTGAGAGCC 1080
QY 1322 AATCATCTTGGCGAACACTCGAGAAAACAGGGGACTAGTACTGTTTATCCGCCATGT 1381
DB 1079 AATCTTCTTGGCGAAAACCGCGAGAAAC--GGGACTAGTACTGTTTGTCCGCCATGT 1022
QY 1382 TAGATTCACCCCACAGGAGTAGCGGCAAGCCGGTAGCGGAGGCTCTTG 1431
DB 1021 TAGATTCACCCCACAGGAGTAGCGGCAAGCTGGCAGCGGAGCGGCTTTG 972

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RESULT 9  
US-09-949-016-12667/c  
; Sequence 12667, Application US/09949016

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12667
; LENGTH: 85152
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-12667

Query Match          49.2%; Score 703.6; DB 3; Length 85152;
Best Local Similarity 85.0%; Pred. No. 1e-210;
Matches 910; Conservative 0; Mismatches 109; Indels 51; Gaps 9;

QY 381 CACAGTTTATTTATCTGTATTTCCAGCTTACTGTGCGACGGA----- 429
DB 2009 CGCAGTTTATTTATCTGTATTTCCCGCTTTCCGTTGCCACGGAACCAAGGGCT 1950
QY 430 ACCGCTGAGCAATAGCCTCTCAGAAATAGAAATCAAGACAGTCAAGAGAGGCGGGA 489
DB 1949 ACCGCTAAGCAGCAGCCTCTCAGAAATAGAAATCAAGGTACATCAGAGATGGAGGGA 1890
QY 490 CAGAAAGAGCCTAGCATCTCTCGGGGCTCTGGGTTGGCCACCAGTCTCCCTGG-TGA 548
DB 1889 CAGAAAGAGCAGCAGTCTCTCGGGGCTCTGATGGCCACCAGTCTGCCCGGAGTA 1830
QY 549 CATAAAAAGAAAGAGAGCGAAAGAAATTTCTACCTGAGTTCCCGTAAAGCGCCGC 608
DB 1829 CGTAAAGAGAAAGAGAGCGAAAGAAATTTCTACCTGAGTTTCCATAAAGTGCCTGC 1770
QY 609 CCTCTGCGCTTACGCTTCCAGTTGCGGCTTATTACGTACAGTAATGCTGTACCAAGG 668
DB 1769 CCTCTAGCCTTACTCTTCCAGTTGCGGCTTATTGATCACAAGTAATGCTGTACGAAG 1710
QY 669 TCAGAAATCGCCACCTGAGGCGCTGAATATCAGCGTAAGATGTCCTCAAGCAAGTCTTAAG 728
DB 1709 TCAGAAATCGCTACC-----TATTGTCCAAAGCAGTCTTAAG 1674
QY 729 AAGAGTCCCATTAACCCCACTCTTCCGCCCTTAATGAGGTCTCCAGTTAGTAAATAA 788
DB 1673 AAGAGTCCCAATCCCCCACTCTTCCGCCCTTAATGAGGTCTCCAGTTAGTAAATAA 1614
QY 789 AAGATGTGTGGAGGTGAGGGAAG-----AACTACTATTTCCTCAATGATGCGGA 843
DB 1613 AAGTAATAGATTTGTTGGGGGGGTGAGGGAATTAATTTTCCAGCATGCGTGGCGGA 1554
QY 844 ACGAAAGCGCTTGGCCCACTGTTCTTGAACCTGAGTGTATGAGAGAGACATCCA 903
DB 1553 ATGAAAGGTCTTCCGCCACAGTGTCTTGAACCTGAGTGTATGAGAGAGACATCCA 1494
QY 904 ATACCAAGCGGCGCACAATTTCTACGGAATTCAGTGATAGATGAGAGAGAGAGAGAGAG 963
DB 1493 ATACCAAGCGGCGCACAATTTCTACGGAATTCAGTGATAGATGAGAGAGAGAGAGAGAG 1434
QY 964 CTATATCATGTCAACAGTAATGAGTTGAGTGTGTTATGTTCTCTATCTTGAAGAGCAG 1023
DB 1433 CTGTACTGTCAACAGTATGAGTGGAG--TGTATGTTTTCGTAATTTGAAAGCAG 1377
QY 1024 AAGACTAGGCCAAAAAGATACCTACAATC-CTAGGAGACTACATTCCTCCATCCAGCC 1082
DB 1376 AACTAGGCTTAAAAAGATACCTACAATCCTTTAGGAGAGACTACATTCCTCCATCCAGCC 1317

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OY	1083	CCACGAGTCTCGGGCAAGTAGTCTCTAAAGTCAGTGCGCTGCCGGGACGCAGTGGCGC	1142
Db	1316	CCAGGAGTCTGGGGCAAGTAGTCTGTAAAGTCAGTGCGCTGCCGGGACGCAGTGAAGCGC	1257
OY	1143	CGAATTTGCTCGGGGAAGGGGAATCCGCTCTGCCCCACAATCGGCACACTCCTAGTTCG	1202
Db	1256	CGAATTTGCTCGGGGCAAGGGGAATCGCTCTGCCCCCATGTCTGCGCACTCGTAGTTCGA	1197
OY	1203	CCCCTCAGCCTCAATGTTTGTATTGTGTGTCGGGTCAGGTGCTTCTGCCCCG-CCCC	1261
Db	1196	CCCCTCAGCCCCCAGTGTGTGTTA--TTTTTCGGGTCAGCTTGCTTTTGCCCCGCTCC	1140
OY	1262	ATCGACGCAATCTCCACCATAATGCGGTGTCGTTTGAAGGACAAGTGATGAGAACC	1321
Db	1139	GTCGACGCAATCGCCACCAATCAATGGGGTGTCGTTTGAAGGACAAGTGATGAGAACC	1080
OY	1322	AATCATCTTGCGGAACATCGGAGAACAAGGGACTAGTTACTGCTTTATCCGCCATGT	1381
Db	1079	AATCTTCTTGCGGAAAAACGGGAGAAAAC--GGGACTAGTTACTGCTTTGTCCGCCATGT	1022
OY	1382	TAGATTCACCCCAACAGGATAGCGGCAAGGCCGCTAGCGGACCGTCTTGG 1431	
Db	1021	TAGATTCACCCCAACAGAGATAGCGGCAAGGCTGGCACGCGGACTTTTG 972	

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RESULT 10
US-09-949-016-12668/c
; Sequence 12668, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12668
; LENGTH: 85152
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12668

Query Match          49.2%; Score 703.6; DB 3; Length 85152;
Best Local Similarity 85.0%; Pred. No. 1e-210;
Matches 910; Conservative 0; Mismatches 109; Indels 51; Gaps 9;

QY      381 CACAGTTTAAATTATCTGTGAATCCCAAGCTTTACTGTTGCCACGGAA----- 429
      |||
DB      2009 CGCAGTTTAAATTATCTGTGAATCCCGCGCTTTCCGTTGCCACGGAAACCAAGGGCT 1950

QY      430 ACCGCTGAGCAATAGCCTCTCAGAAATAGGAATCAAGACACAGTCAGAGGAAGGGCGGGA 489
      |||
DB      1949 ACCGCTTAAAGCAGCAGCCTCTCAGAAATACGAATCAAGGTACAAATCAGAGGATGGGAGGGA 1890

QY      490 CAGAAAGAGCCTAGCATCTCTCGGGGCTCTGGGTTGGCCACCAGTCTCCCTGG-TGA 548
      |||
DB      1889 CAGAAAGAGCCCAAGCGTCTCTCGGGGCTCTGGAATGGCCACCAGTCTGCCCCCGGATGA 1830

QY      549 CATAAAAAGAAAGAGACGGAAGAAAGAAATTTCACTGAGTTCCCGTAAAGCGCCCGC 608
      |||
DB      1829 CGTAAAAAGAAAGAGACGGAAGAGAAAGAAATTTCACTGAGTTTGGCATAAAAGTGCTGC 1770

QY      609 CCTTCGCTCTACGCTTCAGTTGCGGCTTATTAGTCAACAGTAATTGCTGACCAAGG 668
      |||

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Db	1769	CCTTAGCCCTCTACTCTTCCAGTTGCGGCTTATTTGCATCACAAGTAATTTGCTGTACGAAG	1710
Qy	669	TCGAATCGCCACCTGAGGCGCTGAATATCAGCGTAAGATAGTGTCCAAAGCAGTCTTAA	728
Db	1709	TCGAATCGCTACC-----TATTGTCCAAAGCAGTCTTAAG	1674
Qy	729	AAGAGTCCCATTAACCCCACTCTTCCGCCCTAATGAGAGTCTCCAGTTTAAAGTAATA	788
Db	1673	AAGAGTCCCAATCCCCCACTCTTCCGCCCTAATGAGAGTCTCCAGTTTCGTAAATAT	1614
Qy	789	AAGATTTGTTGGAGGTGAGGGAAG-----AACTACTATTTCCAAATGCATGATTGCCGA	843
Db	1613	AAGTAATAAGATTTGTTGGGGGTGAGGGAATAATATTATTTCCAGCATGCTTGCGGA	1554
Qy	844	ACGAAAGGCTTGSCCAACACTGTTCTTTGAAACTGTAGTCTTATGAGAGAAATCCA	903
Db	1553	ATGAAAGGTCTTGCCCAAGTGTCTTTAGAACTGTAGTCTTATGAGAGCAATCCA	1494
Qy	904	ATACCAAGCGGGCAATTTCTACGGAATCCAGTGGATAGATTGAGACCTCCGCGG	963
Db	1493	ATACCAAGCGGGCAATTTCTACGGAATCCAGTGGATAGATTGAGACCTGTGCGG	1434
Qy	964	CTTATCATGTCAACAGTAATGATTGGAGTGTGTTATGTTCTCCATCTTGACAGCAG	1023
Db	1433	CTTGTACTTGTCAACAGTTATGACTGGAG--TGTATGTTTCCGATTTTGAAAGCAG	1377
Qy	1024	AGACTAGGCCCCAAAAAGATACCTACAACCTC-CTAGGAAGACTACGATTCCCATCCAGCC	1082
Db	1376	AAACTAGGCTTTAAAAAGATACGTACAACCTCTTAAAGGAGACTACAATTCATCCAGCC	1317
Qy	1083	CCAGAGTCTCGGGCAAGTAGTCTCTAAGGTCAGTGGCCCTCGGGGACGAGTGGCGC	1142
Db	1316	CCAGAGTCTGGGGCAAGTAGTCTGTAAAGTCAGTGGCCCTCGGGGACGAGTGAAGCGC	1257
Qy	1143	CGAATTTGCTGGGGAAAGGGGAATCCGCTCTGGCCCAATCTGCGCACTCTAGTCCG	1202
Db	1256	CGAATTTGCTGGGGCAGGGGAATGCGTCTGGCCCATGTCTGCGCACTCGTAGTTCCA	1197
Qy	1203	CCCTCAGCCTCAATGTTGTTATTTGTTGTTGTTGCGGTTCAAGTTGCTTTCGCCG-CCCC	1261
Db	1196	CCCTCAGCCTCAAGTTGTTA--TTTTTCGGGTTCAAGTTGCTTTCGCCGCTCC	1140
Qy	1262	ATGACGCAATCTCCACCAATCAATGCGGTGCTGTTTGAGGACAAGTGTGAGACC	1321
Db	1139	GTCGACGCAATCGCCACCAAGTCAATGGGGTGTCTGTTTGAGGACAAGTGTGAGACC	1080
Qy	1322	AATCATCTTGGCGAACAACCTCGGAGAAACAGGGGACTAGTTACTGTCTTATCCGCCATGT	1381
Db	1079	AATCTTCTTGGCGAACAACGCGGAGAAAC--GGGACTAGTTACTGTCTTATCCGCCATGT	1022
Qy	1382	TAGATTACCCCAAGGATAGCGGACAGAGCCGGTAGCGGACGGTCTTTG	1431
Db	1021	TAGATTACCCCAAGAGATAGCGGACAGAGCTGGCAGCGGACGGTCTTTG	972

RESULT 11  
US-09-023-655-887/c  
; Sequence 887, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Selhammer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304





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Db      206 TCCTCCGTGACTGTCACTCTCATCTGTCGACAGATGAGGGCCGAGTAGATGACGGCAGC 147
QY      230 TGGGAGACGAGGCGCCATAGCCGGCGGAGTGTGGGCTGGGGCTGCCGGACGGGTGCTA 289
Db      146 TCGGAGACAGAGGCCATGGCGGGCGGAGTGTAGGGCTGGCGCTGCCGGACGGGTGCTA 87
QY      290 CTCACCGGATGAAGTGAAGGCTCTCACCCCAACGGCGCTTAGCTTCTCGAAGAACCGA 349
Db      86 GTGCGCGGATGAAGTGAAGGCTCTCACCCCAACGGCGCTTAGCTTCTCGAAGAACCGA 27
QY      350 ACACCTTGCGCGGACCGGAGAAAGG 375
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## RESULT 13

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US-09-880-107-2282/c
; Sequence 2282, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2282
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. 6974667 M17886
US-09-880-107-2282
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Query Match      19.5%; Score 279.6; DB 4; Length 512;
Best Local Similarity 91.1%; Pred. No. 8e-78;
Matches 297; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
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QY      50 CCCCCCTTACATGTCAGATGTGGCTCCCAATGTGACGTTGGCCAGGACCTTTGCAAC 109
Db      326 CCGGCCCTTACATGTCAGATGAGGCTCCCAATGTGACGTTGGCCAGGACCTTTGCAAC 267
QY      110 AAGCCAGGCCAAAAGTTTCAATATTACACTGGCTGCTTAATAAGGCAATTGATCTTA 169
Db      266 AAGCCAGGCCAAAAGGCTCAACATTTACACGGCTGCTTAATAAGGCAATTGATCTTA 207
QY      170 TCCTCCGTAAGTTCACCTCATAGTCTGCAATGAGGGCAGAGTAGATGACGCAAGC 229
Db      206 TCCTCCGTAAGTTCACCTCATAGTCTGCAATGAGGGCAGAGTAGATGACGCAAGC 147
QY      230 TGGGAGACGAGGCCATAGCGGGCGGAGTGTGGGCTGGGGCTGCCGGAACGGGTGCTA 289
Db      146 TCGGAGACAGAGGCCATGGCGGGCGGAGTGTAGGGCTGGCGCTGCCGGAACGGGTGCTA 87
QY      290 CTCACCGGATGAAGTGAAGGCTCTCACCCCAACGGCGCTTAGCTTCTCGAAGAACCGA 349
Db      86 GTGCGCGGATGAAGTGAAGGCTCTCACCCCAACGGCGCTTAGCTTCTCGAAGAACCGA 27
QY      350 ACACCTTGCGCGGACCGGAGAAAGG 375
Db      26 GCACCTTGCGCGGACGCTGAGGAAAG 1
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## RESULT 14

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US-09-949-016-15183
; Sequence 15183, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15183
; LENGTH: 9153
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15183
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Best Local Similarity 90.6%; Pred. No. 4.9e-77;
Matches 298; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
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QY      110 AAGCCAGGCCAAAAGTTTCAATATTACACTGGCTGCTTAATAAGGCAATTGATCTTA 169
Db      2211 AAGCCAGGCCAAAAGGTTCAACATTTACACCGGCTGCTTAATAAGGCAATTGATCTTA 2270
QY      170 TCCTCCGTAAGTTCACCTCATAGTCTGCAATGAGGGCAGAGTAGATGACGCAAGC 229
Db      2271 TCCTCCGTAAGTTCACCTCATAGTCTGCAATGAGGGCAGAGTAGATGACGCAAGC 2330
QY      230 TGGGAGACGAGGCCATAGCGGGCGGAGTGTGGGCTGGGGCTGCCGAGCGGTGCTA 289
Db      2331 TGGGAGACGAGGCCATAGCGGGCGGAGTGTGGGCTGGGGCTGCCGAGCGGTGCTA 2390
QY      290 CTCACCGGATGAAGTGAAGGCTCTCACCCCAACGGCGCTTAGCTTCTCGAAGAACCGA 349
Db      2391 GTGCGAGATGAAGTGAAGGCTCTCACCCCAACGGCGCTTAGCTTCTCGAAGAACCGA 2450
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Db      2451 GCACCTTGCGCGGACGCTGAGGAAAGGGGT 2479
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## RESULT 15

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US-09-949-016-15546
; Sequence 15546, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15546
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LENGTH: 187595  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1) .. (187595)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15546

Query Match 17.4%; Score 249.2; DB 3; Length 187595;  
Best Local Similarity 85.3%; Pred. No. 1e-66;  
Matches 278; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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QY 110 AAGCCAGGCCAAAAGTTTCAATATTTACATGGCTGCTTAAAGGGCATTTGATCTTA 169  
DB 172768 AAGCTGACCAAAAAGTTCAACATTTACCAAGCTGCTTAAAGGGCATTTGATCTTA 172827  
QY 170 TCCTCCGTAAGGTCACCTCATAGTCCGCAAGATGAGGCAAGTAGATGCAAGCAAGC 229  
DB 172828 TCCTCCGTAAGGTCACCTCATAGTCCGCAAGATGAGGCAAGTAGATGCAAGCAAGC 172887  
QY 230 TGGAGACGAGGCCCATAGCGCGGCGAGTGTGGGCTGGGGCTGCGGACGCGGTGCTA 289  
DB 172888 TCGGAGACAGAGCATGTATGGGCAAGTGTGGGCTGCGGACGCGGTGCTA 172947  
QY 290 CTCACCGATGAAGTGAGGGTCTCACCCCAACGCGGCTTAGCTTCCTCGAAGACCGA 349  
DB 172948 GTTCCGATGAAGTGAGGGCTCATCCCAAGTGGCTTAGCTTCCTCGAAGACCGA 173007  
QY 350 ACACCTTGGCGGACCGGAAAGG 375  
DB 173008 GCACTGTGTGGCAGCTGAGGAAAGG 173033

Search completed: August 20, 2006, 07:17:13  
Job time : 304 secs



GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2006, 04:46:58 ; Search time 8455 Seconds  
(without alignments)  
10823.035 Million cell updates/sec

Title: US-10-643-829-1

Perfect score: 1431

Sequence: 1 ccgtccagaacgtctcagcg.....ccgttagcgagcgctccttg 1431

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1431	100.0	3800	5	HSU72483	U72483 Human IAI.3
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3	1431	100.0	150582	5	DQ190454	DQ190454 Homo sapi
4	1431	100.0	150669	5	DQ190456	DQ190456 Homo sapi
5	1431	100.0	155470	5	DQ190455	DQ190455 Homo sapi
6	1431	100.0	156121	5	DQ190452	DQ190452 Homo sapi
7	1431	100.0	156879	5	DQ190453	DQ190453 Homo sapi
8	1431	100.0	161765	5	DQ190451	DQ190451 Homo sapi
9	1431	100.0	167910	5	DQ190450	DQ190450 Homo sapi
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11	1381	96.5	1703	5	AY581856	AY581856 Pan trogl
12	1301.8	91.0	1706	5	AY581858	AY581858 Hylobates
13	1165.6	81.5	1688	5	AY581860	AY581860 Papio anu
14	909.4	63.5	1237	2	AR184045	AR184045 Sequence
15	727.6	50.8	1339	5	AY581855	AY581855 Pan trogl
16	727.6	50.8	80966	5	AY365046	AY365046 Pan trogl
17	722.4	50.5	81346	5	AY589042	AY589042 Gorilla g
18	713.6	49.9	83366	5	AY589040	AY589040 Pongo pyg

19	711.2	49.7	1329	5	AY581857	AY581857 Hylobates
20	710.4	49.6	84982	5	AY589041	AY589041 Macaca mu
21	702.2	49.1	1363	5	AY581862	AY581862 Aotus tri
22	702	49.1	6277	2	CQ787189	CQ787189 Sequence
23	702	49.1	6277	2	CQ806564	CQ806564 Sequence
24	702	49.1	6277	2	AX795672	AX795672 Sequence
25	702	49.1	117143	2	CQ776448	CQ776448 Sequence
26	702	49.1	117143	5	L78833	L78833 Homo sapien
27	702	49.1	150472	5	AC135721	AC135721 Homo sapi
28	701	49.0	3798	2	AR380342	AR380342 Sequence
29	701	49.0	3798	5	HSU37574	U37574 Human BRCA1
30	676.8	47.3	1317	5	AY581859	AY581859 Papio anu
31	675.2	47.2	1357	5	AY581861	AY581861 Saginus
32	637.8	44.6	82899	5	AY273801	AY273801 Homo sapi
33	515.4	36.0	174483	12	AC175025	AC175025 Rhinolph
34	512	35.8	4118	5	HSU77841	U77841 Human BRCA1
35	502.6	35.1	143790	12	AC175019	AC175019 Loxodonta
36	494.4	34.5	152765	12	AC174860	AC174860 Sus scrof
37	474.4	33.2	109876	12	AC138235	AC138235 Homo sapi
38	450	31.4	586	5	AF227189	AF227189 Homo sapi
39	450	31.4	4756	2	BD186260	BD186260 STAT6 act
40	446.6	31.2	155192	12	AC172475	AC172475 Bos tauru
41	446.6	31.2	223246	12	AC168285	AC168285 Bos tauru
42	445.2	31.1	111893	12	AC174864	AC174864 Daeypus n
43	443.4	31.0	178489	12	AC174852	AC174852 Oryctolag
44	443.4	31.0	212933	12	AC175004	AC175004 Oryctolag
45	413	28.9	6121	2	AX344396	AX344396 Sequence

ALIGNMENTS

RESULT 1  
HSU72483/c HSU72483 3800 bp DNA linear PRI 22-DEC-1997  
LOCUS Human IAI.3B gene, promoter region.  
DEFINITION U72483  
ACCESSION U72483  
VERSION U72483.1 GI:1771979  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 3800)  
Barker,D.F., Liu,X. and Almeida,E.R.  
TITLE The BRCA1 and IAI.3B promoters are parallel elements of a genomic  
duplication at 17q21  
JOURNAL Genomics 38 (2), 215-222 (1996)  
PUBMED 8954804  
REFERENCE  
2 (bases 1 to 3800)  
Liu,X. and Barker,D.F.  
TITLE Direct Submission  
JOURNAL Submitted (24-SEP-1996) Physiology, University of Utah, 410 Chipeta  
Way, Room 156, Salt Lake City, UT 84108, USA  
FEATURES  
source location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY	61	ATTCCAGATGTGGCTCCCAATGTTGACGCTGGCCAGGACCCTTGCACAAACAGCCAGGCCA	120
Db	1660	ATTGCAGATGTGGCTCCCAATGTTGACGCTGGCCAGGACCCTTGCACAAACAGCCAGGCCA	1601
QY	121	AAAAGTTCAATATTTACACTGGCTCTTAAATAGGGCATTTGATCTTATCTCCGTAAA	180
Db	1600	AAAAGTTCAATATTTACACTGGCTCTTAAATAGGGCATTTGATCTTATCTCCGTAAA	1541
QY	181	GGTCACTCATAGTCCCTGCAGATGAGGGCAGAGTAGATGACAGCAAGCTGGAGACGGA	240
Db	1540	GGTCACTCATAGTCCCTGCAGATGAGGGCAGAGTAGATGACAGCAAGCTGGAGACGGA	1481
QY	241	GGCCATAGCGCGGCGAGTGTGGGGCTGGGGCTGCCGACGCGGTCTACTCACCGGATG	300
Db	1480	GGCCATAGCGCGGCGAGTGTGGGGCTGGGGCTGCCGACGCGGTCTACTCACCGGATG	1421
QY	301	AAGTGAGGCTCAACCCCAACGCGGCTTAGCTTCCCTCGAAGACCGAACACCTTGGCG	360
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QY	361	GCAGCCGAGGAAAGGGGTCCACAGTTTAAATTTATCTGTAAATCCCAAGCTTTACTGT	420
Db	1360	GCAGCCGAGGAAAGGGGTCCACAGTTTAAATTTATCTGTAAATCCCAAGCTTTACTGT	1301
QY	421	GCCACGGAAACCGCTGAGCAATAGCCTCTCAGAAATAGGAAATCAAGACACAGTCAGAGGA	480
Db	1300	GCCACGGAAACCGCTGAGCAATAGCCTCTCAGAAATAGGAAATCAAGACACAGTCAGAGGA	1241
QY	481	AGGGCGGGACAGAAAGAGCCTAGCATCTCTCGGGCTCTGGGTGGCCACCAGTCTCC	540
Db	1240	AGGGCGGGACAGAAAGAGCCTAGCATCTCTCGGGCTCTGGGTGGCCACCAGTCTCC	1181
QY	541	CCTGTGACATAAAAAGAAAGAGACGAAAAAGAAAGTCTACTGAGTTCGCCGTAA	600
Db	1180	CCTGTGACATAAAAAGAAAGAGACGAAAAAGAAAGTCTACTGAGTTCGCCGTAA	1121
QY	601	GCGCCCGCCCTCTCGCCTCTACGCTTCCAGTTGCGGCTTAATACGTACAGTAATTGCTG	660
Db	1120	GCGCCCGCCCTCTCGCCTCTACGCTTCCAGTTGCGGCTTAATACGTACAGTAATTGCTG	1061
QY	661	TACCAAGGTCAGAAATCGCCACTGAGGCTGAATATCAGCGTAAGATAGTGTCCAAAGCA	720
Db	1060	TACCAAGGTCAGAAATCGCCACTGAGGCTGAATATCAGCGTAAGATAGTGTCCAAAGCA	1001
QY	721	GTCCTAAGAAAGGTCCCATTAACCCCACTCTTCCGCCCTAATGAGGTCTCCAGTTTAA	780
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QY	781	GTAATATAAAGATTGTTGGAGGTGAGGGAAGAACTAATTTCCACATGCAATGTC	840
Db	940	GTAATATAAAGATTGTTGGAGGTGAGGGAAGAACTAATTTCCACATGCAATGTC	881
QY	841	GGAACGAAAGCCTTGGCCACACTGTTCTTGAAACTGTAGTCTTATGAGAGAAACAT	900
Db	880	GGAACGAAAGCCTTGGCCACACTGTTCTTGAAACTGTAGTCTTATGAGAGAAACAT	821
QY	901	CCAATACCAAAGCGGGCACAATTTCTCACGGAAATCCAGTGAATAGATTGGAGACCTCCG	960
Db	820	CCAATACCAAAGCGGGCACAATTTCTCACGGAAATCCAGTGAATAGATTGGAGACCTCCG	761
QY	961	GGGCTTATACATGTCAACAGTAATGGAATTGAGTGTGTTATGTTCTCTATCTTGAGAG	1020
Db	760	GGGCTTATACATGTCAACAGTAATGGAATTGAGTGTGTTATGTTCTCTATCTTGAGAG	701
QY	1021	CAGAGACTAGGCCAAAAAAGATACCTACAACCTCTAGGAAGACTACGATTCCATCCAG	1080
Db	700	CAGAGACTAGGCCAAAAAAGATACCTACAACCTCTAGGAAGACTACGATTCCATCCAG	641
QY	1081	CCCCACGAGTCTCGGGCAAGTAGTCTCTTAAGTCAGTGCGCTGCGGGACGCAAGTGGC	1140

D	b		640	CCCCACGAGTCTCGGGCAAGTAGTCCTCTAAGGTACTGCGCCTGCGGGGACGCAGTGGGC	581
O	y		1141	GCCGAATTTGCCCTGGGGAAAGGGGAAATCCGCTCTGGCCCACATCTGCCACTTCTAGTTC	1200
D	b		580	GCCGAATTGCTCTGGGGAAGGGGAAATCCGCTCTGGCCCACATCTGCCACTTCTAGTTC	521
O	y		1201	CGCCCCCAGCCCTCAATGTTGTTATTTGTTGTTCCGGTTCAAGTTGCTTTCGCCCCCCC	1260
D	b		520	CGCCCCCAGCCCTCAATGTTGTTATTTGTTGTTCCGGTTCAAGTTGCTTTCGCCCCCCC	461
O	y		1261	CATGACGCAATCTCCACCAATCAATGGCGTGGTCTTTTGAGGGACAAGTGGTAGAGC	1320
D	b		460	CATGACGCAATCTCCACCAATCAATGGCGTGGTCTTTTGAGGGACAAGTGGTAGAGC	401
O	y		1321	CAATCATCTTGGCGAACACTCGGAGAACAAGGGGACTAGTACTGTCTTAATCCGCATG	1380
D	b		400	CAATCATCTTGGCGAACACTCGGAGAACAAGGGGACTAGTACTGTCTTAATCCGCATG	341
O	y		1381	TTAGATTCACCCCACAGGGATAGCGGCAGAGCCCGTAGCCGACCGTCTTG	1431
D	b		340	TTAGATTCACCCCACAGGGATAGCGGCAGAGCCCGTAGCCGACCGTCTTG	290

RESULT 2  
DQ190457/c

LOCUS DQ190457 147576 bp DNA linear PRI 24-SEP-2005

DEFINITION Homo sapiens clone mck41 A neighbor of BRCA1 gene 1 (NBR1) gene, partial cds; hypothetical protein LOC10230 (NBR2) gene, complete cds; and breast cancer 1 early onset (BRCA1) gene, partial cds.

ACCESSION DQ190457

VERSION DQ190457.1 GI:75875128

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 147576)  
Raymond,C.K., Paddock,M., Subramanian,S., Deodato,C., Zhou,Y., Haugen,B., Kaul,R. and Olson,M.V.  
Direct Submission  
Submitted (01-SEP-2005) Genome Center, Department of Medicine,  
University of Washington, Box 352145, Seattle, WA 98195, USA

TITLE Journal

JOURNAL Direct Submission

FEATURES source location/Qualifiers

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AUTHORS	1 (bases 1 to 150669)
TITLE	Raymond,C.K., Paddock,M., Subramanian,S., Deodato,C., Zhou,Y., Haugen,E., Kaul,R. and Olson,M.V.
JOURNAL	Submitted (01-SEP-2005) Genome Center, Department of Medicine, University of Washington, Box 352145, Seattle, WA 98195, USA
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Raymond,C.K., Paddock,M., Subramanian,S., Deodato,C., Zhou,Y.,  
Haugen,E., Kaul,R. and Olson,M.V.  
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VERSION DQ190452.1 GI:75874674  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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AUTHORS Raymond,C.K., Paddock,M., Subramanian,S., Deodato,C., Zhou,Y., Haugen,E., Kaul,R. and Olson,M.V.  
TITLE Direct Submission  
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VERSION	DQ190453.1	GI:75874793	
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AUTHORS	Raymond,C.K., Paddock,M., Subramanian,S., Deodato,C., Zhou,Y., Haugen,E., Kaul,R. and Olson,M.V.		
TITLE	Submitted (01-SEP-2005) Genome Center, Department of Medicine, University of Washington, Box 352145, Seattle, WA 98195, USA		
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ORIGIN

Query Match 100.0%; Score 1431; DB 5; Length 156879;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	ATTGAGATGTGCTCCCAATGTTGACGTTGGCCAGACCTTTGCA	AACAGCCAGGCCA	120
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QY	241	GGCCATAGCGCGGGAGTGTGGGGCTGCGCGGACGCGGTGCTA	CTCACCAGATG	300
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QY	301	AAGTGAGGTCTCAACCCCAACGCGCCTTAGCTTCTCGAAGAG	ACCGAACACTTGGCG	360
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QY	481	AGGGCGGACAGAAAGAGCCTAGCATCTCTCGGGCTCTGGGTG	GCCACCAAGTCTCTCC	540
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QY	721	GTCTTAAGAAAGGTCCTTACCCCACTCTTCCGCCCTTAATG	AGGTCTCCAGTTTAA	780
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QY	781	GTAATTAAGGATTTGAGAGGTGAGGGAAGAACTACTATTTC	CAACATGCAATTGC	840
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Db	24828	CATGACGCAATCTCCACCAATCAATGGCGGTGCTTTTG	AGGACAAGTGTGAGAGC	24769
QY	1321	CAATCATCTTGGCGAACAACCTCGAGAAACAGGGGACTA	GTTACTGTCTTATCCGCATG	1380
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QY	1381	TTAGATTACCCCAAGGATAGCGGCAAGCCGGTAGCGG	ACGGTCTCTTG	1431
Db	24708	TTAGATTACCCCAAGGATAGCGGCAAGCCGGTAGCGG	ACGGTCTCTTG	24658

RESULT 8  
DQ190451/c 161765 bp DNA linear PRI 24-SEP-2005  
LOCUS DQ190451 Homo sapiens clone mck47 A neighbor of BRCA1 gene 1 (NBR1) gene,  
DEFINITION partial cds; and hypothetical protein LOC10230 (NBR2) and breast  
cancer 1 early onset (BRCA1) genes, complete cds.  
ACCESSION DQ190451  
VERSION DQ190451.1 GI:75874616  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens



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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	
Raymond, C.K., Paddock, M., Subramanian, S., Deodato, C., Zhou, Y., Haugen, E., Kaul, R. and Olson, M.V.	
Submitted (01-SEP-2005) Genome Center, Department of Medicine, University of Washington, Box 352145, Seattle, WA 98195, USA	
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23741	ATTGCAAGTGTGGCTCCCAATGTTGA	CGTTGGCCAGGACCTTTG	CAACAAGCCAGGCCA	23682		
121	AAAAGTTCAATATTACACTGGCTGCTTTA	TAAAGGCAATTGATCTTAT	CCTCCGTAAA	180		
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181	GGTCACTCATAGTCCCTGACAGATGAGGGC	CAGAGTAGATGACGCAAGCTG	GGAGACGA	240		
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361	GCAGCCGAGAAAGGGGTTCCACAGTTTAA	TTTATCTGTAAATCCCAAGCTTTACTGTT	420			
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RESULT 9  
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LOCUS Homo sapiens clone mck432 A neighbor of BRCA1 gene 1 (NBR1) gene,  
DEFINITION partial cds; and hypothetical protein LOC10230 (NBR2) and breast

ACCESSION cancer 1 early onset (BRCA1) genes, complete cds.  
VERSION DQ190450.1 GI:75874526  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 167910)  
AUTHORS Raymond,C.K., Paddock,M., Subramanian,S., Deodato,C., Zhou,Y.,  
Haugen,E., Kaul,R. and Olson,M.V.  
TITLE Direct Submission  
JOURNAL Submitted (01-SEP-2005) Genome Center, Department of Medicine,  
University of Washington, Box 352145, Seattle, WA 98195, USA  
FEATURES  
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location/Qualifiers  
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/product="breast cancer 1 early onset"





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AC060780.18 GI:29126449  
VERSION  
KEYWORDS  
SOURCE  
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Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 110669)  
Birren, B., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome 17, clone RP11-242D8  
Unpublished  
2 (bases 1 to 110669)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Baetien, V., Beda, F.,  
Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,  
Campopiano, A., Caetle, A., Choepel, Y., Colangelo, M., Collins, S.,  
Collamore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Gage, D.,  
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,  
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,  
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,  
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,  
Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N.,  
McCarthy, M., McGowan, P., McGurk, A., McKernan, K., McPheters, R.,  
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,  
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
O'Neil, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,  
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,  
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (20-APR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 110669)  
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
Barna, N., Baetien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,  
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collamore, A.,  
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,  
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,  
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,  
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,  
Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C.,  
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,  
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,  
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,  
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,  
Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P.,  
Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Talamas, J.,  
Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,  
Zembek, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
4 (bases 1 to 110669)  
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
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Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collamore, A.,  
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
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Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,  
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Direct Submission  
Submitted (03-NOV-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
5 (bases 1 to 110669)  
Birren, B., Nusbaum, C., Lander, E., Abouellell, A., Allen, N.,  
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Collamore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,  
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Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,  
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (20-MAR-2003) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 20, 2003 this sequence version replaced gi:24496797.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L7945  
Center clone name: 242\_D\_8  
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Only the first 110.7 kilobases of this clone are being submitted.  
The remainder overlaps accession number AC109326 [WICGR project  
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SOURCE ORGANISM	Pan troglodytes (chimpanzee) Pan troglodytes
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Pan.

REFERENCE	AUTHORS
1 (bases 1 to 1703)	Jin, H., Selfe, J., Whitehouse, C., Morris, J. R., Solomon, E. and Roberts, R. G.

TITLE	Structural evolution of the BRCA1 genomic region in primates
JOURNAL	Genomics 84 (6), 1071-1082 (2004)
PIRMRD	15533724

**AUTHORS** Roberts, R.G., Selfe, J., Jin, H., Whitehouse, C. and Solomon, E.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (18-MAR-2004) Division of Medical and Molecular Sciences

**FEATURES** Location/Qualifiers  
GKT Medical School, 8th Floor, Guy's Tower, Guy's Hospital, London  
SE1 9RT, UK

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REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1237)		
	Holt,J.T., Jensen,R.A., Page,D.L., Obermiller,P.S.,		
	Robinson-Benion,C.L. and Thompson,M.E.		
TITLE	Method for detection and treatment of breast cancer		
JOURNAL	Patent: US 6342483-A 48 29-JAN-2002;		
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Db	371	CCTCTCGCCTCTACGCTTCCAGTTGCGGCTTATTACGTACAGTAATTGCTGTACCAAG	430
QY	669	TCAGAAATCGCAACCTGAGGCTGAATATCAGCGTAAGATAGTGTCCAAAGCAGTCTTAAG	728
Db	431	TCAGAAATCGCAACCTGAGGCTGAATATCAGCGTAAGATAGTGTCCAAAGCAGTCTTAAG	490
QY	729	AAGAGGTCCCAATTACCCCACTCTTCCGCCCTAATGAGGTCCTCAAGTTAGGTAATAA	788
Db	491	AAGAGGTCCCAATTACCCCACTCTTCCGCCCTAATGAGGTCCTCAAGTTAGGTAATAA	550
QY	789	AAGGATGTGGGAGGTGAGGGGAAAGAACTACTATTCCAACATGCATTGCGGAACGA	848
Db	551	AAGGATGTGGGAGGTGAGGGGAAAGAACTACTATTCCAACATGCATTGCGGAACGA	610
QY	849	AGGCTTGGCCACACTGTTCTTGGAAACTGTAGTCTTATGAGAGGAACATCCAAATAC	908

Db	611	AGGCTTGGCCCACTGTTCTCCTTGGAACTGTAGTCTTATGTGAGAGGAACAATCCAATACC	670			
QY	909	AAAGCGGGCACAATTCTCACGGAAATCCAGTGGATAGATTGGAGACCTCCGGGGCTTAT	968			
Db	671	AAAGCGGGCACAATCTCACGGAAATCCAGTGGATAGATTGGAGACCTCCGGGGCTTAT	730			
QY	969	ACATGTCAACAGTAATGGATTGGAGTGTGTTATGTTCTCTATCTTTGAGAGCAGAGACT	1028			
Db	731	ACATGTCAACAGTAA-----TATGGGTGTTATGTTCTCTATCTTTGAGAGCAGAGACT	785			
QY	1029	AGGCCAAAAGATACTACCACTCTAGGAAGACTACGATTCCTATCCAGCCCCACGA	1088			
Db	786	AGGCCAAAAGATA-----TAGGAAGACTACGATTCCTATCCAGCCCCACGA	834			
QY	1089	GTCTCGGGCAAGTAGTCTCTAAGGTCAAGTGGCTCGGGGACGACAGTGGGGCCGAATT	1148			
Db	835	GTCTCGGGCAAGTAGTCTCTAAGGTCAAGTGGCTCGGGGACGACAGTGGGGCCGAATT	894			
QY	1149	TGCCTGGGGAAGGGGAATCCGCTCTGGCCCACATCTGCGCACTCCTAGTTCGGCCCTC	1208			
Db	895	TGCCTGGGGAAGGGGAATCCCTCTCTGTGCATCATCTGCGCACTCCTAGTTCGGCCCTC	954			
QY	1209	AGCCTCAATGTTTGTATTGTTGTTTCGGGTTCAAGGTGCTCTCTGCCCCGCCCATCGACG	1268			
Db	955	AGCATCAATGTTTGTATTGTTGTTTCGGGTTCAAGGTGCTCTCTGCCCCGCCCATCGACG	1014			
QY	1269	CAATCTCCACCAATCAATGCGCTGTCGTTTGAAGGACAAGTGTGAGAGCCATCATC	1328			
Db	1015	CAATCTCCACCAATCAATGCGCTGTCGTTTGAAGGACAAGTGTGAGAGCCATCATC	1074			
QY	1329	TTGCGCAACTCGAGAAACAGGGGACTAGTACTGTCTTATCCGCCATGTAGATTTC	1388			
Db	1075	TTGCGCAACTCGAGAAACAGGGGACTAGTACTGTCTTATCCGCCATGTAGATTTC	1134			
QY	1389	ACCCCAAGGATAGCGCAGAGCCGGTAGCGGACGGTCTTG	1431			
Db	1135	ACCCCAAGGATAGCGCAGAGCCGGTAGCGGACGGTCTTG	1177			
RESULT 15						
AY581855		1339 bp	DNA			
LOCUS	AY581855		linear			
DEFINITION	Pan troglodytes BRCA1-like and NBR2-like genes, complete sequence.					
ACCESSION	AY581855					
VERSION	AY581855.1	GI:51104367				
KEYWORDS	Pan troglodytes (chimpanzee)					
SOURCE	Pan troglodytes					
ORGANISM	Pan troglodytes					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Pan.					
AUTHORS	Jin,H., Selfe,J., Whitehouse,C., Morris,J.R., Solomon,E. and Roberts,R.G.					
TITLE	Structural evolution of the BRCA1 genomic region in primates					
JOURNAL	Genomics 84 (6), 1071-1082 (2004)					
PUBMED	15533724					
REFERENCE	2 (bases 1 to 1339)					
AUTHORS	Roberts,R.G., Selfe,J., Jin,H., Whitehouse,C. and Solomon,E.					
TITLE	Direct Submission					
JOURNAL	Submitted (18-MAR-2004) Division of Medical and Molecular Genetics, GKT Medical School, 8th Floor, Guy's Tower, Guy's Hospital, London SE1 9RT, UK					
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complement(374..377)						
440..609						
/note="similar to Homo sapiens NBR2 exon 1"						
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CAAT_signal						
misc_feature						

CAAT\_signal 1154. .1157  
ORIGIN

Query Match 50.8%; Score 727.6; DB 5; Length 1339;  
Best Local Similarity 85.8%; Pred. No. 5.2e-204;  
Matches 918; Conservative 0; Mismatches 104; Indels 48; Gaps 8;

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QY 381 CACAGTTTAAATTAATCTGTAAATTCACAGCTTAACTGTGGCCACGGAA----- 429
DB 222 CGCAGTTTAAATTAATCTGTAAATTCACAGCTTAACTGTGGCCACGGAAAGGGGCT 281
QY 430 ACCGCTGAGCAATAGCCTCTCAGAAATGAGAAATCAAGACAGTCAAGAGAGGGCGGGA 489
DB 282 ACCGCTAAGCAGCAGCCTCTCAGAAATGAGAAATCAAGTCAATCAGAGATGGAGGGA 341
QY 490 CAGAAAGAGCCTAGCATCTCTGGGGCTCTGGGTTGGCCACCAGTCTCCCTGG-TGA 548
DB 342 CAGAAAGAGCAGCAGCTCTCTGGGGCTCTGGGTTGGCCACCAGTCTCCCTGGATGA 401
QY 549 CATAAAAAGAAAGAGCAGAAAGAGAAATTTACCTGAGTTCCCGTAAAGCCCGGC 608
DB 402 CGTAAAAAGAAAGAGCAGAAAGAGAAATTTACCTGAGTTTGCATAAAGTGCCTGC 461
QY 609 CCTCTCGCCTCTACGCTTCCAGTTGCGGCTTATTAAGTCAAGTAAATTTGCTTACCAAG 668
DB 462 CCTCTAGCCTCTACTCTTCCAGTTGCGGCTTATTAAGTCAAGTAAATTTGCTTACCAAG 521
QY 669 TCAGAAATCGCCACCTGAGGCGCTGAATATCAGCGTAAAGTATGTGCCAAAGCAGTCTTAAG 728
DB 522 TCAGAAATCGCTACC-----TATTTGCCAAAGCAGTCTTAAG 557
QY 729 AAGAGGTCCCATTAACCCCACTCTTCCGCCCTTAAAGAGGTCTCCAGTTTAAATTA 788
DB 558 AAGAGGTCCCATTAACCCCACTCTTCCGCCCTTAAAGAGGTCTCCAGTTTAAATTA 617
QY 789 AAGGATTTGGAGGTGAGGGAAG-----AACTACTATTTCCAAATGCAATGCGGA 843
DB 618 AAGGAATAAGATTTGGGGGGGTGAGGGAATAATATTTCAGCAGTGGCTTGGGA 677
QY 844 ACGAAAGCCTTGGCCACACTGTTCTTGGAACTGTAAGTCTTATGAGAGAAATCCA 903
DB 678 ATGAAGGTCTTCCGCCACAGTGTCTTAAAGTCTTATGAGAGAAATCCA 737
QY 904 ATACCAAGCGGGCAATTTCTACGGAATCCAGTGAATGATTGGAACCTCCCGGG 963
DB 738 ATACCAAGCGGGCAATTTCTACGGAATCCAGTGAATGATTGGAACCTGTGCGG 797
QY 964 CTTATACATGTCAAGTAATGATGAGTGTGTATGTTCTCTATCTTGAGAGCAG 1023
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QY 1024 AGACTAGGCCAAAAAAGATACCTACAATC-CTAGGAAGACTAGATTCCCATCCAGCC 1082
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DB 978 CGAATTTGCTGGGGAAGGGGAATCCGCTTGGCCCAATCTGCGCACTCTAGTTCCG 1037
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DB 1038 CCTCTCAGCCCCCAGTGTGTGA--TTTTCGGGTTCAAGTGTCTTTCGCCGCTCC 1094
QY 1262 ATGACGCAATCTCCAAATCAATGCGTGTCTTTGAGGGAACAAGTGTGAGAGCC 1321
DB 1095 GTCGACGCAATCTCCAAATCAATGCGTGTCTTTGAGGGAACAAGTGTGAGAGCC 1154
QY 1322 AATCATCTTGGGAACACTCGGAGAAACAGGGGACTAGTTACTGTCTTATCCGCATGT 1381
DB 1381 AATCATCTTGGGAACAACCGGAGAAAC--GGACTAGTACTGTCTTATCCGCATGT 1212
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DB 1155 AATCTTCTTGGCGAAAAACGGGAGAAAC--GGACTAGTACTGTCTTATCCGCATGT 1212  
QY 1382 TAGATTCACCCCACAGGATAGCGGCAAGCCGGTAGCGGACGGTCTTG 1431  
DB 1213 TAGATTCACCCCACAGATAGCGGCAAGCTGGCAGCGGACGGTCTTG 1262

Search completed: August 20, 2006, 07:12:06  
Job time : 8459 secs



ID ACC69622 standard; DNA; 2941 BP.  
AC ACC69622;  
XX  
DT 18-JUL-2003 (first entry)  
XX  
DB Human tumour-specific promoter nucleotide sequence SEQ ID NO:1.  
XX  
KW Human; tumour-specific promoter; tumour; cytostatic; ovarian cancer;  
KM gene therapy; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2003025190-A1.  
XX  
PD 27-MAR-2003.  
XX  
PF 30-JAN-2002; 2002WO-JP000724.  
XX  
PR 14-SEP-2001; 2001JP-00279088.  
XX  
PA (PRIM-) PRIMUM KK.  
XX  
PI Hamada K;  
XX  
DR WPI; 2003-313358/30.  
XX  
PT Tumour-specific promoter for producing e.g. transformant adenovirus to  
PT highly proliferate in ovarian cancer cells, applicable in gene therapy  
XX for treating ovarian cancer.  
PS Claim 1; Page 34-36; 41pp; Japanese.  
XX  
CC The present sequence represents a human tumour-specific promoter (I). The  
CC present invention describes the human tumour-specific promoter comprising  
CC bases from 1126-2941 or 2501-2941 in the sequence of (I) with 2941 base  
CC pairs. Also described: (1) another tumour-specific promoter hybridisable  
CC with the specified base sequence under stringent conditions and having a  
CC promoter function as such base sequence; (2) a cytotoxic tumour-specific  
CC promoter to cause specific proliferation in tumour cells or tissue; and  
CC (3) treating tumours by administration of such virus to human. (I) has  
CC cytostatic activity. The promoter can be used for producing e.g.  
CC transformant adenovirus to highly proliferate in ovarian cancer cells,  
CC which is applicable in gene therapy for treating ovarian cancer. When  
CC applied in clinical use, the produced transformant virus has reduced side  
CC effects, and therefore larger quantities can be administered  
XX  
SQ Sequence 2941 BP; 717 A; 825 C; 690 G; 709 T; 0 U; 0 Other;

Query Match 97.2%; Score 1391; DB 8; Length 2941;  
Best Local Similarity 100.0%; Pred. No. 0;  
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DB 1611 ATTGCAGATGTGGCTCCCAATGTTGACGTTGGCCAGACCTTTGCAACAAGCCAGGCCA 1670  
QY 121 AAAAGTTCAATATTATTAAGTCTGCTCTTAATAAGGCAATGATCTTATCTCCGTA 180  
DB 1671 AAAAGTTCAATATTATTAAGTCTGCTCTTAATAAGGCAATGATCTTATCTCCGTA 1730  
QY 181 GGTCACTCATAGTCTCTGAGAGATGAGGCGAGAGATGAGGCAAGCTGGAGACGGA 240  
DB 1731 GGTCACTCATAGTCTCTGAGAGATGAGGCGAGAGATGAGGCAAGCTGGAGACGGA 1790  
QY 241 GGCATATAGCGCGGCGAGAGTGTGGGGCTGGGGCTGGCGGAGCGGGTCTACTACCGGATG 300  
DB 1791 GGCATATAGCGCGGCGAGAGTGTGGGGCTGGGGCTGGCGGAGCGGGTCTACTACCGGATG 1850

QY 301 AAGTGAAGGCTCTACCCCAAGCGGCTTAGCTTCTCGAAGAGACCGAACCCTTGCG 360  
DB 1851 AAGTGAAGGCTCTACCCCAAGCGGCTTAGCTTCTCGAAGAGACCGAACCCTTGCG 1910  
QY 361 GCAGCCGAGAAAGGGGTTCCACAGTTTATTTATTTATTTCCACAGCTTTACTGTT 420  
DB 1911 GCAGCCGAGAAAGGGGTTCCACAGTTTATTTATTTATTTCCACAGCTTTACTGTT 1970  
QY 421 GCCACGGAACCGCTGACGATAGCTCTCAGAAATAGAAATCAAGACACAGTCAGAGA 480  
DB 1971 GCCACGGAACCGCTGACGATAGCTCTCAGAAATAGAAATCAAGACACAGTCAGAGA 2030  
QY 481 AGGGCGGACAGAAAGACCTAGCATCTCTCGGGGCTGTGGTGGCCAGCTCTCC 540  
DB 2031 AGGGCGGACAGAAAGACCTAGCATCTCTCGGGGCTGTGGTGGCCAGCTCTCC 2090  
QY 541 CTTGTGACATTAAGAAAGAGACGGAAGAAAGAAATTTCTACCTGAGTTCCCGTA 600  
DB 2091 CTTGTGACATTAAGAAAGAGACGGAAGAAAGAAATTTCTACCTGAGTTCCCGTA 2150  
QY 601 GCGCCCGCTCTCGCTCTACGCTTCAAGTTGCGGCTTATTAAGTCAAGTAATGCTG 660  
DB 2151 GCGCCCGCTCTCGCTCTACGCTTCAAGTTGCGGCTTATTAAGTCAAGTAATGCTG 2210  
QY 661 TACCAAGTCAAGATTCGCCACCTGAGGCTGAATATCAGCGTAAGATGTCAGAAAGCA 720  
DB 2211 TACCAAGTCAAGATTCGCCACCTGAGGCTGAATATCAGCGTAAGATGTCAGAAAGCA 2270  
QY 721 GTCTTAAGAAAGGTTCCCATTAACCCCTCTTCCGCTTAATGAGGTTCCAGTTAG 780  
DB 2271 GTCTTAAGAAAGGTTCCCATTAACCCCTCTTCCGCTTAATGAGGTTCCAGTTAG 2330  
QY 781 GTAAATTAAGAAAGTGTGGAGGTGAGGAAAGAACTACTATTTCCACATGATTC 840  
DB 2331 GTAAATTAAGAAAGTGTGGAGGTGAGGAAAGAACTACTATTTCCACATGATTC 2390  
QY 841 GGAACGAAAGGCTTGGCCACATCTTCTTGAACCTGTAGTCTTATGAGAGAAAT 900  
DB 2391 GGAACGAAAGGCTTGGCCACATCTTCTTGAACCTGTAGTCTTATGAGAGAAAT 2450  
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Wed Aug 23 08:30:00 2006

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Db 2931 TTAGATTCACC 2941